



RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number:

09/442.489D

Source:

1600

Date Processed by STIC:

9-30-03

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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
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Or
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Revised 04/24/2003

1600

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489D

DATE: 09/30/2003
TIME: 16:00:35

INPUT SET: S37023.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

RECEIVED
OCT 02 2003
TECH CENTER 1600/2900

SEQUENCE LISTING

(1) General Information:

- (i) APPLICANT: ALBERTSEN, HANS
ANAND, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW

VOGELSTEIN, BERT

WHITE, RAYMOND L.

Does Not Comply
Corrected Diskette Needed

(ii) TITLE OF INVENTION: APC ANTIBODIES

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Banner & Allegretti, LTD
(B) STREET: 1001 G Street, NW
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20001-4598

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 09/442,489
(B) FILING DATE: 18-NOV-1999
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/452,654
(B) FILING DATE: 25-MAY-1995

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:36

INPUT SET: S37023.raw

46 (vi) PRIOR APPLICATION DATA:
47 (A) APPLICATION NUMBER: US 08/289,548
48 (B) FILING DATE: 12-AUG-1994
49
50 (vi) PRIOR APPLICATION DATA:
51 (A) APPLICATION NUMBER: US 07/741,940
52 (B) FILING DATE: 08-AUG-1001
53
54
55 (viii) ATTORNEY/AGENT INFORMATION:
56 (A) NAME: Kagan, Sarah A.
57 (B) REGISTRATION NUMBER: 32,141
58 (C) REFERENCE/DOCKET NUMBER: 1107.035574
59
60 (ix) TELECOMMUNICATION INFORMATION:
61 (A) TELEPHONE: 202-508-9100
62 (B) TELEFAX: 202-508-9299
63
64

ERRORED SEQUENCES FOLLOW:

1761 (2) INFORMATION FOR SEQ ID NO:7:
1762
1763 (i) SEQUENCE CHARACTERISTICS:
--> 1764 (A) LENGTH: (2843) amino acids → 2842 amino-acids
1765 (B) TYPE: amino acid
1766 (C) STRANDEDNESS: single
1767 (D) TOPOLOGY: linear
1768
1769 (ii) MOLECULE TYPE: protein
1770
1771 (vi) ORIGINAL SOURCE:
1772 (A) ORGANISM: Homo sapiens
1773
1774 (vii) IMMEDIATE SOURCE:
1775 (B) CLONE: APC
1776
1777
1778
1779 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
1780
1781 Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu
1782 1 5 10 15
1783
1784 Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn
1785 20 25 30
1786
1787 His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu
1788 35 40 45

RAW SEQUENCE LISTING PATENT APPLICATION US/09/442,489D

DATE: 09/30/2003
TIME: 16:00:36

INPUT SET: S37023.raw

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1789
1790      Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly
1791          50                      55                      60
1792
1793      Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser
1794      65                      70                      75                      80
1795
1796      Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr
1797          85                      90                      95
1798
1799      Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro
1800          100                      105                      110
1801
1802      Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg
1803          115                      120                      125
1804
1805      Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu
1806          130                      135                      140
1807
1808      Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala
1809      145                      150                      155                      160
1810
1811      Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Thr Glu Asn
1812          165                      170                      175
1813
1814      Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu Ala
1815          180                      185                      190
1816
1817      Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln Asp
1818          195                      200                      205
1819
1820      Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu
1821          210                      215                      220
1822
1823      Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu
1824      225                      230                      235                      240
1825
1826      Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp Ala
1827          245                      250                      255
1828
1829      Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala Thr
1830          260                      265                      270
1831
1832      Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr Ala
1833          275                      280                      285
1834
1835      Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu Thr
1836          290                      295                      300
1837
1838      Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser Met
1839      305                      310                      315                      320
1840
1841      Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala Met

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/442,489D

DATE: 09/30/2003
TIME: 16:00:36

INPUT SET: S37023.raw

	325	330	335
1842			
1843			
1844	Ser Ser Ser Gln Asp Ser Cys Ile	Ser Met Arg Gln Ser	Gly Cys Leu
1845	340	345	350
1846			
1847	Pro Leu Leu Ile Gln Leu Leu His	Gly Asn Asp Lys Asp Ser Val Leu	
1848	355	360	365
1849			
1850	Leu Gly Asn Ser Arg Gly Ser Lys	Glu Ala Arg Ala Arg Ala Ser Ala	
1851	370	375	380
1852			
1853	Ala Leu His Asn Ile Ile His Ser	Gln Pro Asp Asp Lys Arg Gly Arg	
1854	385	390	395
1855			
1856	Arg Glu Ile Arg Val Leu His Leu	Leu Glu Gln Ile Arg Ala Tyr Cys	
1857	405	410	415
1858			
1859	Glu Thr Cys Trp Glu Trp Gln Glu	Ala His Glu Pro Gly Met Asp Gln	
1860	420	425	430
1861			
1862	Asp Lys Asn Pro Met Pro Ala Pro	Val Glu His Gln Ile Cys Pro Ala	
1863	435	440	445
1864			
1865	Val Cys Val Leu Met Lys Leu Ser	Phe Asp Glu Glu His Arg His Ala	
1866	450	455	460
1867			
1868	Met Asn Glu Leu Gly Gly Leu Gln	Ala Ile Ala Glu Leu Leu Gln Val	
1869	465	470	475
1870			
1871	Asp Cys Glu Met Tyr Gly Leu Thr	Asn Asp His Tyr Ser Ile Thr Leu	
1872	485	490	495
1873			
1874	Arg Arg Tyr Ala Gly Met Ala Leu	Thr Asn Leu Thr Phe Gly Asp Val	
1875	500	505	510
1876			
1877	Ala Asn Lys Ala Thr Leu Cys Ser	Met Lys Gly Cys Met Arg Ala Leu	
1878	515	520	525
1879			
1880	Val Ala Gln Leu Lys Ser Glu Ser	Glu Asp Leu Gln Gln Val Ile Ala	
1881	530	535	540
1882			
1883	Ser Val Leu Arg Asn Leu Ser Trp	Arg Ala Asp Val Asn Ser Lys Lys	
1884	545	550	555
1885			
1886	Thr Leu Arg Glu Val Gly Ser Val	Lys Ala Leu Met Glu Cys Ala Leu	
1887	565	570	575
1888			
1889	Glu Val Lys Lys Glu Ser Thr Leu	Lys Ser Val Leu Ser Ala Leu Trp	
1890	580	585	590
1891			
1892	Asn Leu Ser Ala His Cys Thr Glu	Asn Lys Ala Asp Ile Cys Ala Val	
1893	595	600	605
1894			

RAW SEQUENCE LISTING PATENT APPLICATION US/09/442,489D

DATE: 09/30/2003
TIME: 16:00:36

INPUT SET: S37023.raw

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1895 Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln
1896      610                      615                      620
1897
1898 Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg Asn
1899      625                      630                      635                      640
1900
1901 Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu Arg
1902      645                      650                      655
1903
1904 Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His Ser
1905      660                      665                      670
1906
1907 Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala
1908      675                      680                      685
1909
1910 Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val Ser
1911      690                      695                      700
1912
1913 Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met Gly
1914      705                      710                      715                      720
1915
1916 Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr
1917      725                      730                      735
1918
1919 Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu His
1920      740                      745                      750
1921
1922 Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His Leu
1923      755                      760                      765
1924
1925 Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser His
1926      770                      775                      780
1927
1928 Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe
1929      785                      790                      795                      800
1930
1931 Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly
1932      805                      810                      815
1933
1934 Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser
1935      820                      825                      830
1936
1937 Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp
1938      835                      840                      845
1939
1940 Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His Pro
1941      850                      855                      860
1942
1943 Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser
1944      865                      870                      875                      880
1945
1946 Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala Ile
1947      885                      890                      895

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/442,489D

DATE: 09/30/2003
TIME: 16:00:36

INPUT SET: S37023.raw

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1948
1949 His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu His
1950          900          905          910
1951
1952 Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala His
1953          915          920          925
1954
1955 Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg
1956          930          935          940
1957
1958 Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn
1959          945          950          955          960
1960
1961 Asp Ser Leu Asn Ser Val Ser Ser Ser Asp Gly Tyr Gly Lys Arg Gly
1962          965          970          975
1963
1964 Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys
1965          980          985          990
1966
1967 Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile His
1968          995          1000          1005
1969
1970 Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile
1971          1010          1015          1020
1972
1973 Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln
1974          1025          1030          1035          1040
1975
1976 Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile Glu
1977          1045          1050          1055
1978
1979 Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser Thr
1980          1060          1065          1070
1981
1982 Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys Phe
1983          1075          1080          1085
1984
1985 Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser Arg
1986          1090          1095          1100
1987
1988 Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly Ile
1989          1105          1110          1115          1120
1990
1991 Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu Asp
1992          1125          1130          1135
1993
1994 Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln His
1995          1140          1145          1150
1996
1997 Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu Glu
1998          1155          1160          1165
1999
2000 Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala Thr

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/442,489D

DATE: 09/30/2003
TIME: 16:00:37

INPUT SET: S37023.raw

2001	1170	1175	1180
2002			
2003	Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser Ser		
2004	1185	1190	1195 1200
2005			
2006	Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Ser Glu Asn		
2007		1205	1210 1215
2008			
2009	Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His Pro		
2010		1220	1225 1230
2011			
2012	Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys		
2013		1235	1240 1245
2014			
2015	Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu		
2016		1250	1255 1260
2017			
2018	Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser		
2019		1265	1270 1275 1280
2020			
2021	Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp		
2022		1285	1290 1295
2023			
2024	Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly Thr		
2025		1300	1305 1310
2026			
2027	Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln His		
2028		1315	1320 1325
2029			
2030	Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu		
2031		1330	1335 1340
2032			
2033	Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser Pro		
2034		1345	1350 1355 1360
2035			
2036	Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Val		
2037		1365	1370 1375
2038			
2039	Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser Leu		
2040		1380	1385 1390
2041			
2042	Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu Pro		
2043		1395	1400 1405
2044			
2045	Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp		
2046		1410	1415 1420
2047			
2048	Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro		
2049		1425	1430 1435 1440
2050			
2051	Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys Ala		
2052		1445	1450 1455
2053			

RAW SEQUENCE LISTING PATENT APPLICATION US/09/442,489D

DATE: 09/30/2003
TIME: 16:00:37

INPUT SET: S37023.raw

2054	Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val Asn	
2055	1460	1465 1470
2056		
2057	Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu Leu	
2058	1475	1480 1485
2059		
2060	His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser	
2061	1490	1495 1500
2062		
2063	Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val Glu	
2064	1505	1510 1515 1520
2065		
2066	Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu Thr	
2067	1525	1530 1535
2068		
2069	Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala	
2070	1540	1545 1550
2071		
2072	Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp	
2073	1555	1560 1565
2074	Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro Thr	
2075	1570	1575 1580
2076		
2077	Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu	
2078	1585	1590 1595 1600
2079		
2080	Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu	
2081	1605	1610 1615
2082		
2083	Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe Thr	
2084	1620	1625 1630
2085		
2086	Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro Ile	
2087	1635	1640 1645
2088		
2089	Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro	
2090	1650	1655 1660
2091		
2092	Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln Ser	
2093	1665	1670 1675 1680
2094		
2095	Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr	
2096	1685	1690 1695
2097		
2098	Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu Leu	
2099	1700	1705 1710
2100		
2101	Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn	
2102	1715	1720 1725
2103		
2104	Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys Lys	
2105	1730	1735 1740
2106		

RAW SEQUENCE LISTING PATENT APPLICATION US/09/442,489D

DATE: 09/30/2003
TIME: 16:00:37

INPUT SET: S37023.raw

2107	Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro Asn
2108	1745 1750 1755 1760
2109	
2110	Lys Asn Gln Leu Asp Gly Lys Lys Lys Lys Pro Thr Ser Pro Val Lys
2111	1765 1770 1775
2112	
2113	Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala
2114	1780 1785 1790
2115	
2116	Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn Lys
2117	1795 1800 1805
2118	
2119	Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp
2120	1810 1815 1820
2121	
2122	Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe Asp
2123	1825 1830 1835 1840
2124	
2125	Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser
2126	1845 1850 1855
2127	
2128	Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val Asp
2129	1860 1865 1870
2130	
2131	Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys Glu
2132	1875 1880 1885
2133	
2134	Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln Gln
2135	1890 1895 1900
2136	
2137	Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly
2138	1905 1910 1915 1920
2139	
2140	
2141	Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser
2142	1925 1930 1935
2143	
2144	Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn
2145	1940 1945 1950
2146	
2147	Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser Leu
2148	1955 1960 1965
2149	
2150	Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu
2151	1970 1975 1980
2152	
2153	Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys
2154	1985 1990 1995 2000
2155	
2156	Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp Thr
2157	2005 2010 2015
2158	
2159	Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp

RAW SEQUENCE LISTING PATENT APPLICATION US/09/442,489D

DATE: 09/30/2003
TIME: 16:00:37

INPUT SET: S37023.raw

	2020	2025	2030
2160			
2161			
2162	Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro Lys		
2163	2035	2040	2045
2164			
2165	Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser Pro		
2166	2050	2055	2060
2167			
2168	Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys		
2169	2065	2070	2075 2080
2170			
2171	Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser Glu		
2172	2085	2090	2095
2173			
2174	Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val Ser		
2175	2100	2105	2110
2176			
2177	Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser		
2178	2115	2120	2125
2179			
2180	Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly		
2181	2130	2135	2140
2182			
2183	Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr Ser		
2184	2145	2150	2155 2160
2185			
2186	Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu		
2187	2165	2170	2175
2188			
2189	Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys		
2190	2180	2185	2190
2191			
2192	Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu Ile		
2193	2195	2200	2205
2194			
2195	Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile Ser		
2196	2210	2215	2220
2197			
2198	Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser Ser		
2199	2225	2230	2235 2240
2200			
2201	Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala		
2202	2245	2250	2255
2203			
2204	Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly		
2205	2260	2265	2270
2206			
2207			
2208	Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln Thr		
2209	2275	2280	2285
2210			
2211	Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg		
2212	2290	2295	2300

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:37

INPUT SET: S37023.raw

2213
2214 Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile
2215 2305 2310 2315 2320
2216
2217 Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser
2218 2325 2330 2335
2219
2220 Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr
2221 2340 2345 2350
2222
2223 Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro
2224 2355 2360 2365
2225
2226 Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser
2227 2370 2375 2380
2228
2229 Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu
2230 2385 2390 2395 2400
2231
2232 Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu Ser
2233 2405 2410 2415
2234
2235 Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu
2236 2420 2425 2430
2237
2238 Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser
2239 2435 2440 2445
2240
2241 Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu
2242 2450 2455 2460
2243
2244 Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr
2245 2465 2470 2475 2480
2246
2247 Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His Ser
2248 2485 2490 2495
2249
2250 Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro
2251 2500 2505 2510
2252
2253 Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile Ala
2254 2515 2520 2525
2255
2256 Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly
2257 2530 2535 2540
2258
2259 Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg Val
2260 2545 2550 2555 2560
2261
2262 Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser
2263 2565 2570 2575
2264
2265 Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val Asn

RAW SEQUENCE LISTING PATENT APPLICATION US/09/442,489D

DATE: 09/30/2003
TIME: 16:00:37

INPUT SET: S37023.raw

	2580	2585	2590
2266			
2267			
2268	Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala Lys		
2269	2595	2600	2605
2270			
2271	Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser		
2272	2610	2615	2620
2273			
2274			
2275	Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys		
2276	2625	2630	2635 2640
2277			
2278	Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp Val		
2279	2645	2650	2655
2280			
2281	Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg		
2282	2660	2665	2670
2283			
2284	Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu Lys		
2285	2675	2680	2685
2286			
2287	Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn		
2288	2690	2695	2700
2289			
2290	Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn Arg		
2291	2705	2710	2715 2720
2292			
2293	Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr Glu		
2294	2725	2730	2735
2295			
2296	Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn Glu		
2297	2740	2745	2750
2298			
2299	Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Ser Lys		
2300	2755	2760	2765
2301			
2302	His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe Asn		
2303	2770	2775	2780
2304			
2305	Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg		
2306	2785	2790	2795 2800
2307			
2308	Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg Asp		
2309	2805	2810	2815
2310			
2311	Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg		
2312	2820	2825	2830
2313			
2314	His Ser Gly Ser Tyr Leu Val Thr Ser Val		
2315	2835	2840	
2316			
2317			

total 2842 not 2843

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:38

INPUT SET: S37023.raw

3914
3915 (i) SEQUENCE CHARACTERISTICS:
--> 3916 (A) LENGTH: 24 base pairs 25
3917 (B) TYPE: nucleic acid
3918 (C) STRANDEDNESS: single
3919 (D) TOPOLOGY: linear
3920
3921 (ii) MOLECULE TYPE: cDNA
3922
3923 (vi) ORIGINAL SOURCE:
3924 (A) ORGANISM: Homo sapiens
3925
3926 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:
3927
--> 3928 AGAAGGATCCCTTGTGCAGTGTGGA 25 → All non-coding nucleotides
3929 need to be grouped in 10's (tens)
with a space between each group.

3930 (2) INFORMATION FOR SEQ ID NO:96:
3931
3932 (i) SEQUENCE CHARACTERISTICS:
3933 (A) LENGTH: 24 base pairs
3934 (B) TYPE: nucleic acid
3935 (C) STRANDEDNESS: single
3936 (D) TOPOLOGY: linear
3937
3938 (ii) MOLECULE TYPE: cDNA
3939
3940 (vi) ORIGINAL SOURCE:
--> 3941 (A) Homo sapiens (A) Organism: Homo sapiens. Mandatory
3942 heading missing throughout
3943 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96: sequences.
3944
3945 GACAGGATCCTGAAGCTGAGTTG24 → Same error throughout
3946

3947 (2) INFORMATION FOR SEQ ID NO:97:
3948
3949 (i) SEQUENCE CHARACTERISTICS:
3950 (A) LENGTH: 18 base pairs
3951 (B) TYPE: nucleic acid
3952 (C) STRANDEDNESS: single
3953 (D) TOPOLOGY: linear
3954
3955 (ii) MOLECULE TYPE: cDNA
3956
3957 (vi) ORIGINAL SOURCE:
--> 3958 (A) Homo sapiens
3959
3960 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:
3961
3962 TCAGAAAGTGCTGAAGAG18
3963

3964 (2) INFORMATION FOR SEQ ID NO:98:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:38

INPUT SET: S37023.raw

3965
3966 (i) SEQUENCE CHARACTERISTICS:
3967 (A) LENGTH: 19 base pairs
3968 (B) TYPE: nucleic acid
3969 (C) STRANDEDNESS: single
3970 (D) TOPOLOGY: linear
3971
3972 (ii) MOLECULE TYPE: cDNA
3973
3974 (vi) ORIGINAL SOURCE:
--> 3975 (A) Homo sapiens
3976
3977 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:
3978
3979 GGAATAATTAGGTCTCAA19 *same*
3980

3981 (2) INFORMATION FOR SEQ ID NO:99:
3982
3983 (i) SEQUENCE CHARACTERISTICS:
3984 (A) LENGTH: 21 base pairs
3985 (B) TYPE: nucleic acid
3986 (C) STRANDEDNESS: single
3987 (D) TOPOLOGY: linear
3988
3989 (ii) MOLECULE TYPE: cDNA
3990
3991 (vi) ORIGINAL SOURCE:
--> 3992 (A) Homo sapiens
3993
3994 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
3995
3996 GCAAATCCTAAGAGAGACAA21 *same*
3997

3998 (2) INFORMATION FOR SEQ ID NO:100:
3999
4000 (i) SEQUENCE CHARACTERISTICS:
4001 (A) LENGTH: 19 base pairs
4002 (B) TYPE: nucleic acid
4003 (C) STRANDEDNESS: single
4004 (D) TOPOLOGY: linear
4005
4006 (ii) MOLECULE TYPE: cDNA
4007
4008 (vi) ORIGINAL SOURCE:
--> 4009 (A) Homo sapiens
4010
4011 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:
4012
4013 GATGGCAAGCTTGAGCCAG19 *same*
4014

4015 (2) INFORMATION FOR SEQ ID NO:101:

INPUT SET: S37023.raw

4016
4017 (i) SEQUENCE CHARACTERISTICS:
4018 (A) LENGTH: 18 base pairs
4019 (B) TYPE: nucleic acid
4020 (C) STRANDEDNESS: single
4021 (D) TOPOLOGY: linear
4022
4023 (ii) MOLECULE TYPE: cDNA
4024
4025 (vi) ORIGINAL SOURCE:
--> 4026 (A) Homo sapiens
4027
4028 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
4029
4030 GTTCCAGCAGTGTCACAG18 *same*
4031

4032 (2) INFORMATION FOR SEQ ID NO:102:
4033
4034 (i) SEQUENCE CHARACTERISTICS:
4035 (A) LENGTH: 18 base pairs
4036 (B) TYPE: nucleic acid
4037 (C) STRANDEDNESS: single
4038 (D) TOPOLOGY: linear
4039
4040 (ii) MOLECULE TYPE: cDNA
4041
4042 (vi) ORIGINAL SOURCE:
--> 4043 (A) Homo sapiens
4044
4045 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
4046
--> 4047 GGGAGATTTGCTCCTGA102 *18 group in 10's*
4048
4049

4050 (2) INFORMATION FOR SEQ ID NO:103:
4051
4052 (i) SEQUENCE CHARACTERISTICS:
4053 (A) LENGTH: 23 base pairs
4054 (B) TYPE: nucleic acid
4055 (C) STRANDEDNESS: single
4056 (D) TOPOLOGY: linear
4057
4058 (ii) MOLECULE TYPE: cDNA
4059
4060 (vi) ORIGINAL SOURCE:
--> 4061 (A) Homo sapiens
4062
4063 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
4064
4065 AGTACAAGGA TGCCAATATT ATG
4066

INPUT SET: S37023.raw

4067 (2) INFORMATION FOR SEQ ID NO:104:
4068
4069 (i) SEQUENCE CHARACTERISTICS:
4070 (A) LENGTH: 23 base pairs
4071 (B) TYPE: nucleic acid
4072 (C) STRANDEDNESS: single
4073 (D) TOPOLOGY: linear
4074
4075 (ii) MOLECULE TYPE: cDNA
4076
4077 (vi) ORIGINAL SOURCE:
--> 4078 (A) Homo sapiens
4079
4080 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:
4081
4082 ACTTCTATCT TTTTCAGAAC GAG 23
4083

4084 (2) INFORMATION FOR SEQ ID NO:105:
4085
4086 (i) SEQUENCE CHARACTERISTICS:
4087 (A) LENGTH: 23 base pairs
4088 (B) TYPE: nucleic acid
4089 (C) STRANDEDNESS: single
4090 (D) TOPOLOGY: linear
4091
4092 (ii) MOLECULE TYPE: cDNA
4093
4094 (vi) ORIGINAL SOURCE:
--> 4095 (A) Homo sapiens
4096
4097 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:
4098
4099 ATTTGAATAC TACAGTGTTA CCC 23
4100

4101 (2) INFORMATION FOR SEQ ID NO:106:
4102
4103 (i) SEQUENCE CHARACTERISTICS:
4104 (A) LENGTH: 24 base pairs
4105 (B) TYPE: nucleic acid
4106 (C) STRANDEDNESS: single
4107 (D) TOPOLOGY: linear
4108
4109 (ii) MOLECULE TYPE: cDNA
4110
4111 (vi) ORIGINAL SOURCE:
--> 4112 (A) Homo sapiens
4113
4114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:
4115
4116 CTTGTATTCT AATTGGCAT AAGG 24

INPUT SET: S37023.raw

4117

4118 (2) INFORMATION FOR SEQ ID NO:107:

4119

4120 (i) SEQUENCE CHARACTERISTICS:

4121 (A) LENGTH: 22 base pairs

4122 (B) TYPE: nucleic acid

4123 (C) STRANDEDNESS: single

4124 (D) TOPOLOGY: linear

4125

4126 (ii) MOLECULE TYPE: cDNA

4127

4128 (vi) ORIGINAL SOURCE:

-->

4129 (A) Homo sapiens

4130

4131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

4132

4133 CTGCCCATAC ACATTCAAAC AC

22

4134

4135 (2) INFORMATION FOR SEQ ID NO:108:

4136

4137 (i) SEQUENCE CHARACTERISTICS:

4138 (A) LENGTH: 21 base pairs

4139 (B) TYPE: nucleic acid

4140 (C) STRANDEDNESS: single

4141 (D) TOPOLOGY: linear

4142

4143 (ii) MOLECULE TYPE: cDNA

4144

4145 (vi) ORIGINAL SOURCE:

-->

4146 (A) Homo sapiens

4147

4148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

4149

4150 TGTTTGCGTC TTGCCCATCT T

21

4151

4152 (2) INFORMATION FOR SEQ ID NO:109:

4153

4154 (i) SEQUENCE CHARACTERISTICS:

4155 (A) LENGTH: 24 base pairs

4156 (B) TYPE: nucleic acid

4157 (C) STRANDEDNESS: single

4158 (D) TOPOLOGY: linear

4159

4160 (ii) MOLECULE TYPE: cDNA

4161

4162 (vi) ORIGINAL SOURCE:

-->

4163 (A) Homo sapiens

4164

4165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

4166

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:39

INPUT SET: S37023.raw

4167 AGTCTTAAAT ATTCAGATGA GCAG
4168

24

4169 (2) INFORMATION FOR SEQ ID NO:110:

4170

4171 (i) SEQUENCE CHARACTERISTICS:

4172 (A) LENGTH: 26 base pairs

4173 (B) TYPE: nucleic acid

4174 (C) STRANDEDNESS: single

4175 (D) TOPOLOGY: linear

4176

4177 (ii) MOLECULE TYPE: cDNA

4178

4179 (vi) ORIGINAL SOURCE:

--> 4180 (A) Homo sapiens

4181

4182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

4183

4184 GTTCTCTTC ATTATATTTT ATGCTA

4185

26

4186 (2) INFORMATION FOR SEQ ID NO:111:

4187

4188 (i) SEQUENCE CHARACTERISTICS:

4189 (A) LENGTH: 23 base pairs

4190 (B) TYPE: nucleic acid

4191 (C) STRANDEDNESS: single

4192 (D) TOPOLOGY: linear

4193

4194 (ii) MOLECULE TYPE: cDNA

4195

4196 (vi) ORIGINAL SOURCE:

--> 4197 (A) Homo sapiens

4198

4199 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

4200

4201 AAGCCTACCA ATTATAGTGA ACG

4202

23

4203 (2) INFORMATION FOR SEQ ID NO:112:

4204

4205 (i) SEQUENCE CHARACTERISTICS:

4206 (A) LENGTH: 23 base pairs

4207 (B) TYPE: nucleic acid

4208 (C) STRANDEDNESS: single

4209 (D) TOPOLOGY: linear

4210

4211 (ii) MOLECULE TYPE: cDNA

4212

4213 (vi) ORIGINAL SOURCE:

--> 4214 (A) Homo sapiens

4215

4216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

INPUT SET: S37023.raw

4217
4218 AGCTGATGAC AAAGATGATA ATC 23
4219

4220 (2) INFORMATION FOR SEQ ID NO:113:

4221

4222 (i) SEQUENCE CHARACTERISTICS:

4223 (A) LENGTH: 24 base pairs

4224 (B) TYPE: nucleic acid

4225 (C) STRANDEDNESS: single

4226 (D) TOPOLOGY: linear

4227

4228 (ii) MOLECULE TYPE: cDNA

4229

4230 (vi) ORIGINAL SOURCE:

--> 4231 (A) Homo sapiens

4232

4233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

4234

4235 AAGAAACAAT ACAGACTTAT TGTG 24

4236

4237 (2) INFORMATION FOR SEQ ID NO:114:

4238

4239 (i) SEQUENCE CHARACTERISTICS:

4240 (A) LENGTH: 20 base pairs

4241 (B) TYPE: nucleic acid

4242 (C) STRANDEDNESS: single

4243 (D) TOPOLOGY: linear

4244

4245 (ii) MOLECULE TYPE: cDNA

4246

4247 (vi) ORIGINAL SOURCE:

--> 4248 (A) Homo sapiens

4249

4250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

4251

4252 ATGAGTGGGG TCTCCTGAAC 20

4253

4254 (2) INFORMATION FOR SEQ ID NO:115:

4255

4256 (i) SEQUENCE CHARACTERISTICS:

4257 (A) LENGTH: 21 base pairs

4258 (B) TYPE: nucleic acid

4259 (C) STRANDEDNESS: single

4260 (D) TOPOLOGY: linear

4261

4262 (ii) MOLECULE TYPE: cDNA

4263

4264 (vi) ORIGINAL SOURCE:

--> 4265 (A) Homo sapiens

4266

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:39

INPUT SET: S37023.raw

4267 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:
4268
4269 ATCTCCCTCC AAAAGTGGTG C
4270

21

4271 (2) INFORMATION FOR SEQ ID NO:116:
4272

4273 (i) SEQUENCE CHARACTERISTICS:
4274 (A) LENGTH: 22 base pairs
4275 (B) TYPE: nucleic acid
4276 (C) STRANDEDNESS: single
4277 (D) TOPOLOGY: linear
4278

4279 (ii) MOLECULE TYPE: cDNA
4280

4281 (vi) ORIGINAL SOURCE:

--> 4282 (A) Homo sapiens

4283

4284 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

4285

4286 TCCATCTGGA GTACTTCTG TG
4287

22

4288 (2) INFORMATION FOR SEQ ID NO:117:
4289

4290 (i) SEQUENCE CHARACTERISTICS:
4291 (A) LENGTH: 22 base pairs
4292 (B) TYPE: nucleic acid
4293 (C) STRANDEDNESS: single
4294 (D) TOPOLOGY: linear
4295

4296 (ii) MOLECULE TYPE: cDNA
4297

4298 (vi) ORIGINAL SOURCE:

--> 4299 (A) Homo sapiens

4300

4301 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

4302

4303 AGTAAATGCT GCAGTTCAGA GG
4304

22

4305 (2) INFORMATION FOR SEQ ID NO:118:
4306

4307 (i) SEQUENCE CHARACTERISTICS:
4308 (A) LENGTH: 19 base pairs
4309 (B) TYPE: nucleic acid
4310 (C) STRANDEDNESS: single
4311 (D) TOPOLOGY: linear
4312

4313 (ii) MOLECULE TYPE: cDNA
4314

4315 (vi) ORIGINAL SOURCE:

--> 4316 (A) Homo sapiens

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:39

INPUT SET: S37023.raw

4317
4318 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:
4319
4320 CCGTGGCATA TCATCCCCC
4321

19

4322 (2) INFORMATION FOR SEQ ID NO:119:
4323
4324 (i) SEQUENCE CHARACTERISTICS:
4325 (A) LENGTH: 22 base pairs
4326 (B) TYPE: nucleic acid
4327 (C) STRANDEDNESS: single
4328 (D) TOPOLOGY: linear
4329
4330 (ii) MOLECULE TYPE: cDNA
4331
4332 (vi) ORIGINAL SOURCE:
--> 4333 (A) Homo sapiens
4334
4335 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
4336 CCCAGACTGC TTCAAATTA CC
4337

22

4338 (2) INFORMATION FOR SEQ ID NO:120:
4339
4340 (i) SEQUENCE CHARACTERISTICS:
4341 (A) LENGTH: 21 base pairs
4342 (B) TYPE: nucleic acid
4343 (C) STRANDEDNESS: single
4344 (D) TOPOLOGY: linear
4345
4346 (ii) MOLECULE TYPE: cDNA
4347
4348 (vi) ORIGINAL SOURCE:
--> 4349 (A) Homo sapiens
4350
4351 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:
4352
4353 GAGCCTCATC TGTACTTCTG C
4354

21

4355 (2) INFORMATION FOR SEQ ID NO:121:
4356
4357 (i) SEQUENCE CHARACTERISTICS:
4358 (A) LENGTH: 21 base pairs
4359 (B) TYPE: nucleic acid
4360 (C) STRANDEDNESS: single
4361 (D) TOPOLOGY: linear
4362
4363 (ii) MOLECULE TYPE: cDNA
4364
4365 (vi) ORIGINAL SOURCE:
--> 4366 (A) Homo sapiens

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:39

INPUT SET: S37023.raw

4367
4368 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:
4369
4370 CCCTCCAAAT GAGTTAGCTG C
4371

21

4372 (2) INFORMATION FOR SEQ ID NO:122:
4373
4374 (i) SEQUENCE CHARACTERISTICS:
4375 (A) LENGTH: 23 base pairs
4376 (B) TYPE: nucleic acid
4377 (C) STRANDEDNESS: single
4378 (D) TOPOLOGY: linear
4379
4380 (ii) MOLECULE TYPE: cDNA
4381
4382 (vi) ORIGINAL SOURCE:
--> 4383 (A) Homo sapiens
4384
4385 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:
4386
4387 TTGTGGTATA GGTTTTACTG GTG
4388

23

4389 (2) INFORMATION FOR SEQ ID NO:123:
4390
4391 (i) SEQUENCE CHARACTERISTICS:
4392 (A) LENGTH: 23 base pairs
4393 (B) TYPE: nucleic acid
4394 (C) STRANDEDNESS: single
4395 (D) TOPOLOGY: linear
4396
4397 (ii) MOLECULE TYPE: cDNA
4398
4399 (vi) ORIGINAL SOURCE:
--> 4400 (A) Homo sapiens
4401
4402 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:
4403
4404 ACCCAACAAA AATCAGTTAG ATG
4405

23

4406 (2) INFORMATION FOR SEQ ID NO:124:
4407
4408 (i) SEQUENCE CHARACTERISTICS:
4409 (A) LENGTH: 21 base pairs
4410 (B) TYPE: nucleic acid
4411 (C) STRANDEDNESS: single
4412 (D) TOPOLOGY: linear
4413
4414 (ii) MOLECULE TYPE: cDNA
4415
4416 (vi) ORIGINAL SOURCE:

INPUT SET: S37023.raw

--> 4417 (A) Homo sapiens
4418
4419 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:
4420
4421 GTGGCTGGTA ACTTTAGCCT C
4422

21

4423 (2) INFORMATION FOR SEQ ID NO:125:

4424

4425 (i) SEQUENCE CHARACTERISTICS:

4426 (A) LENGTH: 21 base pairs

4427 (B) TYPE: nucleic acid

4428 (C) STRANDEDNESS: single

4429 (D) TOPOLOGY: linear

4430

4431 (ii) MOLECULE TYPE: cDNA

4432

4433 (vi) ORIGINAL SOURCE:

--> 4434 (A) Homo sapiens

4435

4436 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

4437

4438 ATGATGTTGA CCTTCCAGG G

4439

21

4440 (2) INFORMATION FOR SEQ ID NO:126:

4441

4442 (i) SEQUENCE CHARACTERISTICS:

4443 (A) LENGTH: 24 base pairs

4444 (B) TYPE: nucleic acid

4445 (C) STRANDEDNESS: single

4446 (D) TOPOLOGY: linear

4447

4448 (ii) MOLECULE TYPE: cDNA

4449

4450 (vi) ORIGINAL SOURCE:

--> 4451 (A) Homo sapiens

4452

4453 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

4454

4455 ATTGTGTAAC TTTTCATCAG TTGC

4456

24

4457 (2) INFORMATION FOR SEQ ID NO:127:

4458

4459 (i) SEQUENCE CHARACTERISTICS:

4460 (A) LENGTH: 21 base pairs

4461 (B) TYPE: nucleic acid

4462 (C) STRANDEDNESS: single

4463 (D) TOPOLOGY: linear

4464

4465 (ii) MOLECULE TYPE: cDNA

4466

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:40

INPUT SET: S37023.raw

4467 (vi) ORIGINAL SOURCE:
--> 4468 (A) Homo sapiens
4469
4470 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:
4471
4472 AAAGACATAC CAGACAGAGG G 21
4473

4474 (2) INFORMATION FOR SEQ ID NO:128:
4475
4476 (i) SEQUENCE CHARACTERISTICS:
4477 (A) LENGTH: 21 base pairs
4478 (B) TYPE: nucleic acid
4479 (C) STRANDEDNESS: single
4480 (D) TOPOLOGY: linear
4481
4482 (ii) MOLECULE TYPE: cDNA
4483
4484 (vi) ORIGINAL SOURCE:
--> 4485 (A) Homo sapiens
4486
4487 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:
4488
4489 CTTTTTTGGC ATTGCGGAGC T 21
4490

4491 (2) INFORMATION FOR SEQ ID NO:129:
4492
4493 (i) SEQUENCE CHARACTERISTICS:
4494 (A) LENGTH: 22 base pairs
4495 (B) TYPE: nucleic acid
4496 (C) STRANDEDNESS: single
4497 (D) TOPOLOGY: linear
4498
4499 (ii) MOLECULE TYPE: cDNA
4500
4501 (vi) ORIGINAL SOURCE:
--> 4502 (A) Homo sapiens
4503
4504 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:
4505
4506 AAGATGACCT GTTGCAGGAA TG 22
4507

4508 (2) INFORMATION FOR SEQ ID NO:130:
4509
4510 (i) SEQUENCE CHARACTERISTICS:
4511 (A) LENGTH: 24 base pairs
4512 (B) TYPE: nucleic acid
4513 (C) STRANDEDNESS: single
4514 (D) TOPOLOGY: linear
4515
4516 (ii) MOLECULE TYPE: cDNA

INPUT SET: S37023.raw

4517
4518 (vi) ORIGINAL SOURCE:
--> 4519 (A) Homo sapiens
4520
4521 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:
4522
4523 GAATCAGACC AAGCTTGTCT AGAT
4524 24

4525 (2) INFORMATION FOR SEQ ID NO:131:
4526
4527 (i) SEQUENCE CHARACTERISTICS:
4528 (A) LENGTH: 24 base pairs
4529 (B) TYPE: nucleic acid
4530 (C) STRANDEDNESS: single
4531 (D) TOPOLOGY: linear
4532
4533 (ii) MOLECULE TYPE: cDNA
4534
4535 (vi) ORIGINAL SOURCE:
--> 4536 (A) Homo sapiens
4537
4538 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:
4539
4540 CAATAGTAAG TAGTTTACAT CAAG
4541 24

4542 (2) INFORMATION FOR SEQ ID NO:132:
4543
4544 (i) SEQUENCE CHARACTERISTICS:
4545 (A) LENGTH: 22 base pairs
4546 (B) TYPE: nucleic acid
4547 (C) STRANDEDNESS: single
4548 (D) TOPOLOGY: linear
4549
4550 (ii) MOLECULE TYPE: cDNA
4551
4552 (vi) ORIGINAL SOURCE:
--> 4553 (A) Homo sapiens
4554
4555 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:
4556
4557 AAACAGGACT TGTACTGTAG GA
4558 22

4559 (2) INFORMATION FOR SEQ ID NO:133:
4560
4561 (i) SEQUENCE CHARACTERISTICS:
4562 (A) LENGTH: 21 base pairs
4563 (B) TYPE: nucleic acid
4564 (C) STRANDEDNESS: single
4565 (D) TOPOLOGY: linear
4566

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:40

INPUT SET: S37023.raw

4567 (ii) MOLECULE TYPE: cDNA
4568
4569 (vi) ORIGINAL SOURCE:
--> 4570 (A) Homo sapiens
4571
4572 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:
4573
4574 CAGCCCCCTTC AAGCAAACAT C 21
4575

4576 (2) INFORMATION FOR SEQ ID NO:134:
4577
4578 (i) SEQUENCE CHARACTERISTICS:
4579 (A) LENGTH: 22 base pairs
4580 (B) TYPE: nucleic acid
4581 (C) STRANDEDNESS: single
4582 (D) TOPOLOGY: linear
4583
4584 (ii) MOLECULE TYPE: cDNA
4585
4586 (vi) ORIGINAL SOURCE:
--> 4587 (A) Homo sapiens
4588
4589 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:
4590
4591 GAGGACTTAT TCCATTTCTA CC 22
4592

4593 (2) INFORMATION FOR SEQ ID NO:135:
4594
4595 (i) SEQUENCE CHARACTERISTICS:
4596 (A) LENGTH: 20 base pairs
4597 (B) TYPE: nucleic acid
4598 (C) STRANDEDNESS: single
4599 (D) TOPOLOGY: linear
4600
4601 (ii) MOLECULE TYPE: cDNA
4602
4603 (vi) ORIGINAL SOURCE:
--> 4604 (A) Homo sapiens
4605
4606 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:
4607
4608 CAGTCTCCTG GCCGAAACTC 20
4609

4610 (2) INFORMATION FOR SEQ ID NO:136:
4611
4612 (i) SEQUENCE CHARACTERISTICS:
4613 (A) LENGTH: 22 base pairs
4614 (B) TYPE: nucleic acid
4615 (C) STRANDEDNESS: single
4616 (D) TOPOLOGY: linear

INPUT SET: S37023.raw

4617
4618 (ii) MOLECULE TYPE: cDNA
4619
4620 (vi) ORIGINAL SOURCE:
--> 4621 (A) Homo sapiens
4622
4623 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:
4624
4625 GTTGACTGGC GTACTAATAC AG
4626 22

4627 (2) INFORMATION FOR SEQ ID NO:137:
4628
4629 (i) SEQUENCE CHARACTERISTICS:
4630 (A) LENGTH: 23 base pairs
4631 (B) TYPE: nucleic acid
4632 (C) STRANDEDNESS: single
4633 (D) TOPOLOGY: linear
4634
4635 (ii) MOLECULE TYPE: cDNA
4636
4637 (vi) ORIGINAL SOURCE:
--> 4638 (A) Homo sapiens
4639
4640 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:
4641
4642 TGGTAATGGA GCCAATAAAA AGG
4643 23

4644 (2) INFORMATION FOR SEQ ID NO:138:
4645
4646 (i) SEQUENCE CHARACTERISTICS:
4647 (A) LENGTH: 20 base pairs
4648 (B) TYPE: nucleic acid
4649 (C) STRANDEDNESS: single
4650 (D) TOPOLOGY: linear
4651
4652 (ii) MOLECULE TYPE: cDNA
4653
4654 (vi) ORIGINAL SOURCE:
--> 4655 (A) Homo sapiens
4656
4657 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:
4658
4659 TGGGACTTTT CGCCATCCAC
4660 20

4661 (2) INFORMATION FOR SEQ ID NO:139:
4662
4663 (i) SEQUENCE CHARACTERISTICS:
4664 (A) LENGTH: 22 base pairs
4665 (B) TYPE: nucleic acid
4666 (C) STRANDEDNESS: single

INPUT SET: S37023.raw

4667 (D) TOPOLOGY: linear
4668
4669 (ii) MOLECULE TYPE: cDNA
4670
4671 (vi) ORIGINAL SOURCE:
--> 4672 (A) Homo sapiens
4673
4674 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:
4675
4676 TGTCTCTATC CACACATTCG TC 22
4677

4678 (2) INFORMATION FOR SEQ ID NO:140:
4679
4680 (i) SEQUENCE CHARACTERISTICS:
4681 (A) LENGTH: 24 base pairs
4682 (B) TYPE: nucleic acid
4683 (C) STRANDEDNESS: single
4684 (D) TOPOLOGY: linear
4685
4686 (ii) MOLECULE TYPE: cDNA
4687
4688 (vi) ORIGINAL SOURCE:
--> 4689 (A) Homo sapiens
4690
4691 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:
4692
4693 ATGTTTTTCA TCCTCACTTT TTGC 24
4694

4695 (2) INFORMATION FOR SEQ ID NO:141:
4696
4697 (i) SEQUENCE CHARACTERISTICS:
4698 (A) LENGTH: 22 base pairs
4699 (B) TYPE: nucleic acid
4700 (C) STRANDEDNESS: single
4701 (D) TOPOLOGY: linear
4702
4703 (ii) MOLECULE TYPE: cDNA
4704
4705 (vi) ORIGINAL SOURCE:
--> 4706 (A) Homo sapiens
4707
4708 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:
4709
4710 GGAGAAGAAC TGGAAGTTCA TC 22
4711

4712 (2) INFORMATION FOR SEQ ID NO:142:
4713
4714 (i) SEQUENCE CHARACTERISTICS:
4715 (A) LENGTH: 25 base pairs
4716 (B) TYPE: nucleic acid

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:41

INPUT SET: S37023.raw

4717 (C) STRANDEDNESS: single
4718 (D) TOPOLOGY: linear
4719
4720 (ii) MOLECULE TYPE: cDNA
4721
4722 (vi) ORIGINAL SOURCE:
--> 4723 (A) Homo sapiens
4724
4725 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:
4726
4727 TTGAATCTTT AATGTTTGA TTTGC
4728 25

4729 (2) INFORMATION FOR SEQ ID NO:143:
4730
4731 (i) SEQUENCE CHARACTERISTICS:
4732 (A) LENGTH: 21 base pairs
4733 (B) TYPE: nucleic acid
4734 (C) STRANDEDNESS: single
4735 (D) TOPOLOGY: linear
4736
4737 (ii) MOLECULE TYPE: cDNA
4738
4739 (vi) ORIGINAL SOURCE:
--> 4740 (A) Homo sapiens
4741
4742 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:
4743
4744 TCTCCCACAG GTAATACTCC C
4745 21

4746 (2) INFORMATION FOR SEQ ID NO:144:
4747
4748 (i) SEQUENCE CHARACTERISTICS:
4749 (A) LENGTH: 21 base pairs
4750 (B) TYPE: nucleic acid
4751 (C) STRANDEDNESS: single
4752 (D) TOPOLOGY: linear
4753
4754 (ii) MOLECULE TYPE: cDNA
4755
4756 (vi) ORIGINAL SOURCE:
--> 4757 (A) Homo sapiens
4758
4759 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:
4760
4761 GCTACAACTG AATGGGGTAC G
4762 21

4763 (2) INFORMATION FOR SEQ ID NO:145:
4764
4765 (i) SEQUENCE CHARACTERISTICS:
4766 (A) LENGTH: 22 base pairs

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:41

INPUT SET: S37023.raw

4767 (B) TYPE: nucleic acid
4768 (C) STRANDEDNESS: single
4769 (D) TOPOLOGY: linear
4770
4771 (ii) MOLECULE TYPE: cDNA
4772
4773 (vi) ORIGINAL SOURCE:
--> 4774 (A) Homo sapiens
4775
4776 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:
4777
4778 CAGGACAAAA TAATCCTGTC CC 22
4779

4780 (2) INFORMATION FOR SEQ ID NO:146:
4781
4782 (i) SEQUENCE CHARACTERISTICS:
4783 (A) LENGTH: 24 base pairs
4784 (B) TYPE: nucleic acid
4785 (C) STRANDEDNESS: single
4786 (D) TOPOLOGY: linear
4787
4788 (ii) MOLECULE TYPE: cDNA
4789
4790 (vi) ORIGINAL SOURCE:
--> 4791 (A) Homo sapiens
4792
4793 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:
4794
4795
4796 ATTTTCTTAC TTTCATTCTT CCTC 24
4797

4798 (2) INFORMATION FOR SEQ ID NO:147:
4799
4800 (i) SEQUENCE CHARACTERISTICS:
4801 (A) LENGTH: 20 amino acids
4802 (B) TYPE: amino acid
4803 (D) Topology: mandatory heading missing throughout
4804 (ii) MOLECULE TYPE: protein amino acid sequences
4805
4806 (vi) ORIGINAL SOURCE:
--> 4807 (A) Artificial sequence (consensus)
4808
--> 4809 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:
4810
4811 Phe Xaa Val Glu Xaa Thr Pro Xaa Cys Phe Ser Arg Xaa Ser Ser Leu Ser Ser Leu
4812 1 5 10 15
4813
4814 Ser
4815 20
4816

4817 (2) INFORMATION FOR SEQ ID NO:148:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:41

INPUT SET: S37023.raw

4818
4819 (i) SEQUENCE CHARACTERISTICS:
4820 (A) LENGTH: 20 amino acids
4821 (B) TYPE: amino acid
4822 (D) *same*
4823 (ii) MOLECULE TYPE: protein
4824
4825 (vi) ORIGINAL SOURCE:
--> 4826 (A) Homo sapiens
4827
--> 4828 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:
4829
4830 Tyr Cys Val Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu
4831 1 5 10 15
4832 Ser Ser Leu Ser
4833 20
4834

4835 (2) INFORMATION FOR SEQ ID NO:149:
4836
4837 (i) SEQUENCE CHARACTERISTICS:
4838 (A) LENGTH: 20 amino acids
4839 (B) TYPE: amino acid
4840 (D)
4841 (ii) MOLECULE TYPE: protein
4842
4843 (vi) ORIGINAL SOURCE:
--> 4844 (A) Homo sapiens
4845
--> 4846 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:
4847
4848 His Thr Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val
4849 1 5 10 15
4850 Ser Ser Leu Asp
4851 20
4852

4853 (2) INFORMATION FOR SEQ ID NO:150:
4854
4855 (i) SEQUENCE CHARACTERISTICS:
4856 (A) LENGTH: 20 amino acids
4857 (B) TYPE: amino acid
4858 (D)
4859 (ii) MOLECULE TYPE: protein
4860
4861 (vi) ORIGINAL SOURCE:
--> 4862 (A) Homo sapiens
4863
--> 4864 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:
4865
4866 Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser Leu
4867 1 5 10 15
4868 Ser Ala Leu Ser

INPUT SET: S37023.raw

4869 20
4870

4871 (2) INFORMATION FOR SEQ ID NO:151:
4872
4873 (i) SEQUENCE CHARACTERISTICS:
4874 (A) LENGTH: 20 amino acids
4875 (B) TYPE: amino acid
4876 (D)
4877 (ii) MOLECULE TYPE: protein
4878
4879 (vi) ORIGINAL SOURCE:
--> 4880 (A) Homo sapiens
4881
--> 4882 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:
4883
4884 Tyr Cys Val Glu Gly Thr Pro Ile Asn Phe Ser Thr Ala Thr Ser Leu
4885 1 5 10 15
4886 Ser Asp Leu Thr
4887 20
4888

4889 (2) INFORMATION FOR SEQ ID NO:152:
4890
4891 (i) SEQUENCE CHARACTERISTICS:
4892 (A) LENGTH: 20 amino acids
4893 (B) TYPE: amino acid
4894 (D)
4895 (ii) MOLECULE TYPE: protein
4896
4897 (vi) ORIGINAL SOURCE:
--> 4898 (A) Homo sapiens
4899
--> 4900 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:
4901
4902 Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser Arg Asn Asp Ser Leu
4903 1 5 10 15
4904 Ser Ser Leu Asp
4905 20
4906

4907 (2) INFORMATION FOR SEQ ID NO:153:
4908
4909 (i) SEQUENCE CHARACTERISTICS:
4910 (A) LENGTH: 20 amino acids
4911 (B) TYPE: amino acid
4912 (D)
4913 (ii) MOLECULE TYPE: protein
4914
4915 (vi) ORIGINAL SOURCE:
--> 4916 (A) Homo sapiens
4917
--> 4918 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,489DDATE: 09/30/2003
TIME: 16:00:42

INPUT SET: S37023.raw

4919
4920 Phe Ala Ile Glu Asn Thr Pro Val Cys Pro Ser His Asn Ser Ser Leu
4921 1 5 10 15
4922 Ser Ser Leu Ser
4923 20
4924

4925 (2) INFORMATION FOR SEQ ID NO:154:

4926

4927 (i) SEQUENCE CHARACTERISTICS:

4928 (A) LENGTH: 20 amino acids

4929 (B) TYPE: amino acid

4930

4931 (ii) MOLECULE TYPE: protein

4932

4933 (vi) ORIGINAL SOURCE:

--> 4934 (A) Homo sapiens

4935

--> 4936 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

4937

4938 Arg His Val Glu Asp Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu

4939 1 5 10 15

4940 Ser Ser Leu Ser

4941 20

4942

--> 4943 ?? delete

4944

4945

4946

4947

4948

4949

4950

4951

4952

4953

4954
